IN THE CLAIMS

Please amend the claims as follows:

1-29. (Canceled)

30. (Currently Amended) A process for the production of a ~~*Haemophilus influenzae* specific~~ lipooligosaccharide (LOS) which comprises the steps of:

(a) growing in a culture medium *Salmonella minnesota* ~~gram-negative~~ bacteria comprising (i) a core lipid structure containing a terminal heptose and (ii) a DNA sequence encoding an Undecaprenyl-phosphate N-acetyl glucosaminyl phosphate transferase (*rfe*), and (iii) an isolated DNA sequence encoding a lipooligosaccharide-synthesis gene G polypeptide (LsgG) from *Haemophilus influenzae*, wherein the DNA sequence encoding *rfe* is regulated by LsgG such that the ~~a *H. influenzae* specific~~ LOS is synthesized by the addition of an acceptor molecule to the terminal heptose molecule; and

(b) recovering the ~~*H. influenzae* specific~~ LOS from the culture medium.

Claims 31-33. (Cancelled)

34. (Previously presented) The process of claim 30, wherein the acceptor molecule is N-acetylglucosamine.

Claims 35-36. (Cancelled).

37. (Previously presented) The process of claim 30, wherein the isolated DNA sequence encoding the LsgG is comprised in a vector.

38. (Previously presented) The process of claim 30, wherein the bacteria further comprise a glycosyltransferase.

39. (Currently amended) A process for the production of a complex carbohydrate comprising the steps of:

(a) growing in a culture medium *Salmonella minnesota* ~~gram-negative~~ bacteria comprising (i) a core lipid structure containing a terminal heptose and (ii) a DNA sequence encoding an Undecaprenyl-phosphate N-acetyl glucosaminyl phosphate transferase (*rfe*), and (iii) an isolated DNA sequence encoding a lipooligosaccharide-synthesis gene G polypeptide (LsgG) from *Haemophilus influenzae*, wherein the DNA sequence encoding *rfe* is regulated by LsgG such that a complex carbohydrate is synthesized by the addition of an acceptor molecule to the heptose molecule; and

(b) recovering the complex carbohydrate from the culture medium.

Claims 40-42. (Cancelled)

43. (Previously presented) The process of claim 39, wherein the acceptor molecule is N-acetylglucosamine.

Claims 44-45. (Cancelled)

46. (Previously presented) The process of claim 39, wherein the isolated DNA sequence encoding LsgG is contained in a vector.

47. (Previously presented) The process of claim 39, wherein the bacteria further comprise a glycosyltransferase.

48. (Currently amended) A method comprising modifying a terminal heptose of a lipopolysaccharide (LPS) or lipooligosaccharide (LOS) core structure of a *Salmonella minnesota* bacterium ~~gram-negative bacterial species~~, wherein the bacterium ~~gram-negative bacterial species~~ comprises a polynucleotide encoding an Undecaprenyl-phosphate N-acetyl glucosaminyl phosphate transferase (*rfe*) and an isolated DNA sequence encoding a lipooligosaccharide-synthesis gene G polypeptide (LsgG) from

Haemophilus influenzae, wherein the polynucleotide encoding *rfe* is regulated by lipooligosaccharide-synthesis gene G polypeptide (LsgG) from *Haemophilus influenzae* such that an N-acetyl glucosamine is added onto the terminal heptose so as to modify the terminal heptose~~, wherein the gram-negative bacterial species is *Salmonella minnesota*~~.

Claims 49-53. (Cancelled)

54. (Previously presented) The method of claim 48, wherein a polynucleotide encoding the LsgG is comprised in a vector.

55. (Previously presented) The method of claim 48, wherein the bacteria further comprise a glycosyltransferase.

56. (Previously presented) The process of claim 38, wherein the glycosyltransferase is a *Haemophilus influenzae* glycosyltransferase.

57. (Previously presented) The process of claim 47, wherein the glycosyltransferase is a *Haemophilus influenzae* glycosyltransferase.

58. (Previously presented) The method of claim 55, wherein the glycosyltransferase is a *Haemophilus influenzae* glycosyltransferase.